- (1) GENERAL INFORMATION:
- (i) APPLICANT: Barbas III, Carlos F. Gottesfeld, Joel M. Wright, Peter E.
- (ii) TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
- (iii) NUMBER OF SEQUENCES: 62
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Fish & Richardson P.C.
  - (B) STREET: 4225 Executive Square, Suite 1400
  - (C) CITY: La Jolla
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: Windows 95
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/863,813
  - (B) FILING DATE: 27-MAY-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/676,318
  - (B) FILING DATE: 18-JUL-1996
  - (A) APPLICATION NUMBER: 08/183,119
  - (B) FILING DATE: 18-JAN-1996
  - (A) APPLICATION NUMBER: US95/00829
  - (B) FILING DATE: 18-JAN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Haile, Lisa A., Ph.D.
  - (B) REGISTRATION NUMBER: 38,347
  - (C) REFERENCE/DOCKET NUMBER: 08401/010001
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 619/678-5070
  - (B) TELEFAX: 619/678-5099
  - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (B) LOCATION: 1...1
  - (D) OTHER INFORMATION: wher Xaa at position is Tyr or Phe

- (B) LOCATION: 2, 4-7, 9-11, 13-17, 19, 22-25, and 27-32
  (D) OTHER INFORMATION: where Xaa at the above positions is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa at positions 6 or 7 may be missing; Xaa at position 25 may be missing; Xaa at positions 29, 30, 31, or 32 may be missing
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: ZF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAAACTGC TCGAGCCCTA TGCTTGCCCT GTCGAG

36

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: ZR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGGAGGAGG AGACTAGTGT CCTTCTGTCT TAAATGGATT TTGGT

45

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 273 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: zif268Xho-Spe
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...273

	( )	(i) S	EQUE	ENCE	DESC	RIPT	:NOI	SEÇ	ID.	NO:4	:					
CTC Leu 1	GAG Glu	CCC Pro	TAT Tyr	GCT Ala 5	TGC Cys	CCT Pro	GTC Val	GAG Glu	TCC Ser 10	TGC Cys	GAT Asp	CGC Arg	CGC Arg	TTT Phe 15	TCT Ser	48
CGC Arg	TCG Ser	GAT Asp	GAG Glu 20	CTT Leu	ACC Thr	CGC Arg	CAT His	ATC Ile 25	CGC Arg	ATC Ile	CAC His	ACA Thr	GGC Gly 30	CAG Gln	AAG Lys	96
CCC Pro	TTC Phe	CAG Gln 35	TGT Cys	CGA Arg	ATA Ile	TGC Cys	ATG Met 40	CGT Arg	AAC Asn	TTC Phe	AGT Ser	CGT Arg 45	AGT Ser	GAC Asp	CAC His	144
CTT Leu	ACC Thr 50	ACC Thr	CAC His	ATC Ile	CGC Arg	ACC Thr 55	CAC His	ACA Thr	GGC Gly	GAG Glu	AAG Lys 60	CCT Pro	TTT Phe	GCC Ala	TGT Cys	192
GAC Asp 65	ATT Ile	ТGT	GGG Gly	AGG Arg	AAG Lys 70	TTT Phe	GCC Ala	AGG Arg	AGT Ser	GAT Asp 75	GAA Glu	CGC Arg	AAG Lys	AGG Arg	CAT His 80	240
ACC Thr	AAA Lys	ATC Ile	CAT His	TTA Leu 85	AGA Arg	CAG Gln	AAG Lys	GAC Asp	ACT Thr 90	AGT Ser						273

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 91 amino acids (B) TYPE: amino acid

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser 10 1 Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys 25 20 Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His 35 40 Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys 55 50 Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His 80 75 70 65 Thr Lys Ile His Leu Arg Gln Lys Asp Thr Ser 85

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: FTX3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
GCAATTAACC CTCACTAAAG GG	22
(2) INFORMATION FOR SEQ ID NO:7:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(vii) IMMEDIATE SOURCE: (B) CLONE: BZF3	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
GGCAAACTTC CTCCCACAAA T	21
(2) INFORMATION FOR SEQ ID NO:8:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	:
(vii) IMMEDIATE SOURCE: (B) CLONE: ZF36K	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
ATTTGTGGGA GGAAGTTTGC CNNKAGTNNK NNKNNKNNKN NKCATACCAA AATCCATTTA	60
(2) INFORMATION FOR SEQ ID NO:9:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(vii) IMMEDIATE SOURCE: (B) CLONE: R3B	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
TTGATATTCA CAAACGAATG G	21
(2) INFORMATION FOR SEQ ID NO:10:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	

(B) CLONE: ZFNsi-B	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
CATGCATATT CGACACTGGA A	21
(2) INFORMATION FOR SEQ ID NO:11:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 66 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	•
(ii) MOLECULE TYPE: Genomic DNA	
(vii) IMMEDIATE SOURCE: (B) CLONE: ZF2r6F	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
CAGTGTCGAA TATGCATGCG TAACTTCNNK NNKNNKNNKN NKNNKACCAC CACCAC	CCACATCCGC 60 66
(2) INFORMATION FOR SEQ ID NO:12:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 66 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(vii) IMMEDIATE SOURCE: (B) CLONE: AFI6rb	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
CTGGCCTGTG TGGATGCGGA TATGMNNMNN MNNMNNMNNC GAMNNAGAAA 3 GCAGGA	AGCGGCGATC 60
(2) INFORMATION FOR SEQ ID NO:13:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 24 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(vii) IMMEDIATE SOURCE: (B) CLONE: ZFIF	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
CATATCCGCA TCCACACAGG CCAG	24
(2) INFORMATION FOR SEQ ID NO:14:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 amino acids	

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Ser Asp Glu Leu Thr Arg His

- (2) INFORMATION FOR SEQ ID NO:15:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser Arg Ser Asp His Leu
1 5

- (2) INFORMATION FOR SEQ ID NO:16:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGTAAATGGG CGCCCTTTTG GGCGCCCATT TACG

- (2) INFORMATION FOR SEQ ID NO:17:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Ser Asp Glu Arg Lys Arg His

- (2) INFORMATION FOR SEQ ID NO:18:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

34

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
- Trp Ser Ile Pro Val Leu Leu His
  - (2) INFORMATION FOR SEQ ID NO:19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 8 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp Ser Leu Leu Pro Val Leu His

- (2) INFORMATION FOR SEQ ID NO:20:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Phe Ser Phe Leu Leu Pro Leu His

- (2) INFORMATION FOR SEQ ID NO:21:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Ser Thr Trp Arg Gly Trp His

- (2) INFORMATION FOR SEQ ID NO:22:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Ser Ile Gln Leu Pro Tyr His

- (2) INFORMATION FOR SEQ ID NO:23:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGATCTCAGA AGCCAAGCAG GGTCGGGCCT GGTTAGTACT TGGATGGGAG ACCGCCTGGG

60 61

- (2) INFORMATION FOR SEQ ID NO: 24:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Tyr Ile Cys Ser Phe Ala Asp Cys Gly Ala Ala Tyr Asn Lys Asn Trp Lys Leu Gln Ala His Leu Cys Lys His Thr 20

- (2) INFORMATION FOR SEQ ID NO:25:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Phe Pro Cys Lys Glu Glu Gly Cys Glu Lys Gly Phe Thr Ser Leu His His Leu Thr Arg His Ser Leu Thr His Thr 20

- (2) INFORMATION FOR SEQ ID NO:26:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Phe Thr Cys Asp Ser Asp Gly Cys Asp Leu Arg Phe Thr Thr Lys Ala 15 Asn Met Lys Lys His Phe Asn Arg Phe His 20

(2) INFORMATION FOR SEQ ID NO:27:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 13 bas pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
TGGATGGGAG ACC	13
(2) INFORMATION FOR SEQ ID NO:28:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 8 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: peptide	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
Arg Ser Asp Glu Arg Lys Arg His 1 5	
(2) INFORMATION FOR SEQ ID NO:29:	:
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
GTCCATAAGA TTAGCGGATC C	21
(2) INFORMATION FOR SEQ ID NO:30:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
GTGAGCGAGG AAGCGGAAGA G	21
(2) INFORMATION FOR SEQ ID NO:31:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 34 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single	

	(11)	ODDC.						-				•			
	(xi) S	EQUE	NCE I	DESC	RIPT	ion:	SEQ	ID I	NO: 3	1:					
CCTGCG	TGGG (	GCCC	rttt(	G GG	CGCC	CACG	CAG	G							34
	(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	NO: 3	2:						
	(B)	QUENG LENG TYPE TOPO	TH: 4	4 am	ino a acid	acid	CS: s								
	(ii) 1	COLEC	ULE '	TYPE	: pe	ptid	е				•				
	(ix)   (B (D	LOC	ATIO	N: 4 NFOR	4 MATI	ON:	wher	e Xa	a at	pos	itio	n 4	is L	ys oı	r Pro
	(xi)	SEQUE	NCE :	DESC	RIPT	ion:	SEQ	ID	NO:3	2:					
Thr Gl	y Glu	Xaa													
•	. 12	) INF	ORMA	TION	FOR	SEO	ID	NO: 3	3:						
	•	•													
	(B)	LENG TYPE STRA TOPO	TH: : nu NDED	462 clei NESS	base c ac : si	pai id ngle	rs.								
	(ii)	MOLEC	ULE	TYPE	: Ge	nomi	.c DN	IA							
	(ix) (A (B	FEATU ) NAM ) LOC	Œ/KE	Y: C N: 1	Codin	ıg S∈ 159	equer	ıce							
	(xi)	SEQUE	ENCE	DESC	RIPT	: NOI	SEÇ	] ID	NO:3	33:					
ATG CT Met Le	TC GAG eu Glu	CTC Leu	CCC Pro 5	TAT Tyr	GCT Ala	TGC Cys	CCT Pro	GTC Val 10	GAG Glu	TCC Ser	TGC Cys	GAT Asp	CGC Arg 15	CGC Arg	48
TTT TO	CT CGC er Arg	TCG Ser 20	GAT Asp	GAG Glu	CTT Leu	ACC Thr	CGC Arg 25	CAT His	ATC Ile	CGC Arg	ATC Ile	CAC His 30	ACA Thr	GGC Gly	96
CAG A	AG CCC ys Pro	Phe	CAG Gln	TGT Cys	CGA Arg	ATA Ile 40	TGC Cys	ATG Met	CGT Arg	AAC Asn	TTC Phe 45	AGT Ser	CGT Arg	AGT Ser	144
Asp H	AC CTI is Lev	ACC Thr	ACC Thr	CAC His	ATC Ile 55	CGC Arg	ACC Thr	CAC His	ACA Thr	GGC Gly 60	GAG Glu	AAG Lys	CCT Pro	TTT Phe	192
GCC TO Ala C 65	GT GAG	ATT Ile	TGT Cys	GGG Gly 70	AGG Arg	AAG Lys	TTT Phe	GCC Ala	AGG Arg 75	AGT Ser	GAT Asp	GAA Glu	CGC Arg	AAG Lys 80	240
AGG C Arg H	AT AC	AAA Lys	ATC	CAT His	ACC Thr	GGR Xaa	CAG Gln	AAG Lys	Pro	ACT Thr	AGT Ser	GGC Gly	GGT Gly	Gly	288

C( A)	g	ATC Ile	GCC Ala	CGG Arg 100	CTG Leu	GAG Glu	GAA Glu	AAA Lys	GTG Val 105	AAA Lys	ACC Thr	TTG Leu	AAA Lys	GCG Ala 110	CAA Gln	AAC Asn	336
TO	CC er	GAG Glu	CTG Leu 115	GCG Ala	TCC Ser	ACC Thr	CGG Arg	AAC Asn 120	ATG Met	CTC Leu	AGG Arg	GAA Glu	CAG Gln 125	GTG Val	GCA Ala	CAG Gln	384
C:	rT eu	AAA Lys 130	CAG Gln	AAA Lys	GTC Val	ATG Met	AAC Asn 135	CAC His	GCT Ala	AGC Ser	GGC Gly	CAG Gln 140	GCC Ala	GGC Gly	CAG Gln	TAC Tyr	432
P							TAC Tyr			TAA							462

# (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg 10 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly 25 20 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser 40 Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe 60 55 Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys 70 Arg His Thr Lys Ile His Thr Xaa Gln Lys Pro Thr Ser Gly Gly 90 Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn 105 100 Ser Glu Leu Ala Ser Thr Arg Asn Met Leu Arg Glu Gln Val Ala Gln 120 125 115 Leu Lys Gln Lys Val Met Asn His Ala Ser Gly Gln Ala Gly Gln Tyr 140 130 Pro Tyr Asp Val Pro Asp Tyr Ala Ser 150

### (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 462 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...459

	( х	i) S	EQUE	INCE	DESC	KILI	: TON:	SEG	עד נ	NO						
ATG Met 1	CTC Leu	GAG Glu	CTC Leu	CCC Pro 5	TAT Tyr	GCT Ala	TGC Cys	CCT Pro	GTC Val 10	GAG Glu	TCC Ser	TGC Cys	GAT Asp	CGC Arg 15	CGC Arg	48
TTT Phe	TCT Ser	CGC Arg	TCG Ser 20	GAT Asp	GAG Glu	CTT Leu	ACC Thr	CGC Arg 25	CAT His	ATC Ile	CGC Arg	ATC Ile	CAC His 30	ACA Thr	GGC Gly	<sub>.</sub> 96
CAG Gln	AAG Lys	CCC Pro 35	TTC Phe	CAG Gln	TGT Cys	CGA Arg	ATA Ile 40	TGC Cys	ATG Met	CGT Arg	AAC Asn	TTC Phe 45	AGT Ser	CGT Arg	AGT Ser	144
GAC Asp	CAC His 50	CTT Leu	ACC Thr	ACC Thr	CAC His	ATC Ile 55	CGC Arg	ACC Thr	CAC His	ACA Thr	GGC Gly 60	GAG Glu	AAG Lys	CCT Pro	TTT Phe	192
GCC Ala 65	TGT Cys	GAC Asp	ATT Ile	TGT Cys	GGG Gly 70	AGG Arg	AAG Lys	TTT Phe	GCC Ala	AGG Arg 75	AGT Ser	GAT Asp	GAA Glu	CGC Arg	AAG Lys 80	240
AGG Arg	CAT His	ACC Thr	AAA Lys	ATC Ile 85	CAT His	ACC Thr	GGT Gly	CAG Gln	AAG Lys 90	CCC Pro	ACT Thr	AGT Ser	GGC Gly	GGT Gly 95	GGT Gly	288
CTG Leu	ACC Thr	GAC Asp	ACC Thr 100	CTG Leu	CAG Gln	GCG Ala	GAA Glu	ACC Thr 105	Asp	CAG Gln	CTG Leu	GAA Glu	GAC Asp 110	GIu	AAA Lys	336
TCC	GCG Ala	CTG Leu 115	Gln	ACC Thr	GAA Glu	ATC Ile	GCG Ala 120	Asn	CTG Leu	CTG Leu	AAA Lys	GAA Glu 125	Lys	GAA Glu	AAG Lys	384
CTG Leu	GAG Glu 130	Phe	ATC Ile	CTG Leu	GCG Ala	GCA Ala 135	His	GCT Ala	AGC Ser	GGC Gly	CAG Gln 140	Ala	GGC	CAG Gln	TAC Tyr	432
	Tyr		GTT Val			Tyr										462

# (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

 Met
 Leu
 Glu
 Leu
 Pro
 Tyr
 Ala
 Cys
 Pro
 Val
 Glu
 Ser
 Cys
 Arg
 Arg
 Inches
 Inch

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys 65 70 75 80

Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly Gly 85 90 95

Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys 100

Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys 115

Leu Glu Phe Ile Leu Ala Ala His Ala Ser Gly Gln Ala Gly Gln Tyr 130

Pro Tyr Asp Val Pro Asp Tyr Ala Ser 150

- (2) INFORMATION FOR SEQ ID NO:37:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

#### CGCCCACGCN GCGTGGGCG

19

- (2) INFORMATION FOR SEQ ID NO:38:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

### CGCCCACGCN GCGGCGGCG CGGCGGCG

28

- (2) INFORMATION FOR SEQ ID NO:39:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (B) LOCATION: 76...76
- (D) OTHER INFORMATION: where Xaa at position 76 is Tyr-Ala-Cys-Pro-Val-Glu-Ser-Cys-Asp-Arg-Phe-Ser-Lys-Ser-Ala-Asp-Leu-Lys-His-Ile-Arg-His-Thr-Gly-Glu-Lys-Pro-Met-Lys-Leu-Leu-Glu-Pro-repeated 10 times; residue 76=340 amino acids; some Xaa's may be missing
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg
1 5 10 15

Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg His Thr Gly
20 25 30

Thr Thr

,																
Glu	Lys		Met :	Lys :	Leu l	Leu (	Glu :	Pro '	Tyr	Ala	Сув	Pro '	Val	Glu	Ser	
Сув	Asp	35 Arg	Arg :	Phe	Ser 1	Lys :	40 Ser	Ala :	Asp :	Leu	Lys 1		Ile	Arg	His	
_	50		•		Met 1 70	55					60					•
		(2)	INF	ORMA	TION	FOR	SEQ	ID	NO: 4	0:						
	(i	(A) (B) (C)	LENG TYPE STRA	TH: : nu NDED	HARA 34 b clei NESS : li	ase c ac : si	pair id ngle	8								
	i)	.i) M	OLEC	ULE	TYPE	: Ge	nomi	.c DN	Ά							
	(2	ri) S	EQUE	NCE	DESC	RIPT	'ION:	SEQ	ID	NO:4	10:					
CCT	cgccc	cc e	CGGG	TTTT	c cc	GCGC	cccc	GAG	G							34
		(2)	INF	ORMA	TION	FOR	SEÇ	Q ID	NO:4	1:						
	( :	(A) (B) (C)	LENG TYPE STRA	TH: : nu NDED	HARA 293 Iclei NESS	base c ac	pai id ngle	irs								
	(:	ii) 1	COLEC	CULE	TYPE	: G∈	enomi	LC DN	IA				*			
	(i:	(A)	EATUF ) NAM ) LOC	Œ/KI	EY: C	odir	ng Se 294	equer	ıce							
	(:	xi)	SEQUI	ENCE	DESC	RIPT	CION	: SEÇ	Q ID	NO:	41:					•
ATG Met 1	Lys	CTG Leu	CTC Leu	GAG Glu 5	CCC Pro	TAT Tyr	GCT Ala	TGC Cys	CCT Pro 10	GTC Val	GAG Glu	TCC Ser	TGC Cys	GAT Asp 15	CGC Arg	48
CGC Arg	TTT Phe	TCT Ser	AAG Lys 20	Ser	GCT Ala	GAT Asp	CTG Leu	AAG Lys 25	CGC Arg	CAT His	ATC Ile	CGC Arg	ATC Ile 30	CAC His	ACT Thr	96
GGC Gly	GAA Glu	AAA Lys 35	Pro	TAC Tyr	GCG Ala	TGC Cys	CCT Pro 40	Val	GAG Glu	TCC Ser	TGC Cys	GAT Asp 45	CGC Arg	CGC Arg	TTT Phe	144
TCT Ser	AAG Lys	Ser	GCT Ala	GAT Asp	CTG Leu	AAG Lys 55	CGC Arg	CAT	ATC Ile	CGC Arg	ATC Ile 60	CAC His	ACC	GGG Gly	GAG Glu	192
AAG	ccc	TAT	GCT	TGC	CCT	GTC	GAG	TCC	TGC	GAT	CGC	CGC	TTT	TCT	AAG	240

Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Gln Lys Pro 95 85 ACT AC

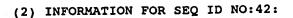
Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Lys
65 70 75 80

TCG GCT GAT CTG AAG CGC CAT ATC CGC ATC CAC ACC GGT CAG AAG CCC

70

293

288



# (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

 Met
 Lys
 Leu
 Leu
 Glu
 Pro
 Tyr
 Ala
 Cys
 Pro
 Val
 Glu
 Ser
 Cys
 Asp
 Leu
 Lys
 Arg
 His
 Ile
 Arg
 Ile
 His
 Thr

 Gly
 Glu
 Lys
 Pro
 Tyr
 Ala
 Cys
 Pro
 Val
 Glu
 Ser
 Cys
 Asp
 Arg
 Phe

 Ser
 Lys
 Ser
 Ala
 Asp
 Leu
 Lys
 Arg
 His
 Ile
 Arg
 Arg
 Arg
 Phe

 Lys
 Pro
 Tyr
 Ala
 Cys
 Pro
 Val
 Glu
 Ser
 Cys
 Asp
 Arg
 Phe
 Ser
 Lys
 Arg
 His
 Ile
 His
 Thr
 Glu
 Ser
 Lys
 Arg
 Phe
 Ser
 Lys
 Arg
 His
 Ile
 His
 Thr
 Glu
 Ser
 Lys
 Arg
 His
 Thr
 Glu
 Thr
 Glu

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 543 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...543
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATG Met 1	CTC Leu	GAG Glu	CTC Leu	CCC Pro 5	TAT Tyr	GCT Ala	TGC Cys	CCT Pro	GTC Val 10	GAG Glu	TCC Ser	TGC Cys	GAT Asp	CGC Arg 15	CGC Arg	48
TTT Phe	TCT Ser	CGC Arg	TCG Ser 20	GAT Asp	GAG Glu	CTT Leu	ACC Thr	CGC Arg 25	CAT His	ATC Ile	CGC Arg	ATC Ile	CAC His 30	ACA Thr	GGC Gly	96
CAG Gln	AAG Lys	CCC Pro 35	TTC Phe	CAG Gln	TGT Cys	CGA Arg	ATA Ile 40	TGC Cys	ATG Met	CGT Arg	AAC Asn	TTC Phe 45	AGT Ser	CGT Arg	AGT Ser	144
GAC Asp	CAC His 50	Leu	ACC Thr	ACC Thr	CAC His	ATC Ile 55	CGC Arg	ACC Thr	CAC His	ACA Thr	GGC Gly 60	GAG Glu	AAG Lys	CCT Pro	TTT Phe	192
GCC Ala 65	Сув	GAC Asp	ATT Ile	TGT Cys	GGG Gly 70	AGG Arg	AAG Lys	TTT Phe	GCC Ala	AGG Arg 75	AGT Ser	GAT Asp	GAA Glu	CGC Arg	AAG Lys 80	240

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AGG Arg	CAT His	ACC Thr	AAA Lys	ATC Ile 85	CAT His	ACC Thr	GGG Gly	GAG Glu	AAG Lys 90	CCC Pro	TAT Tyr	GCT Ala	TGC Cys	CCT Pro 95	GTC Val	288
GAG Glu	TCC Ser	TGC Cys	GAT Asp 100	CGC Arg	CGC Arg	TTT Phe	TCT Ser	CGC Arg 105	TCG Ser	GAT Asp	GAG Glu	CTT Leu	ACC Thr 110	CGC Arg	CAT His	336
ATC Ile	CGC Arg	ATC Ile 115	CAC His	ACA Thr	GGC Gly	CAG Gln	AAG Lys 120	CCC Pro	TTC Phe	CAG Gln	TGT Cys	CGA Arg 125	ATA Ile	TCC Ser	ATG Met	384
CGT Arg	AAC Asn 130	TTC Phe	AGT Ser	CGT Arg	AGT Ser	GAC Asp 135	CAC His	CTT Leu	ACC Thr	ACC Thr	CAC His 140	ATC Ile	CGC Arg	ACC Thr	CAC His	432
ACA Thr 145	GGC Gly	GAG Glu	AAG Lys	CCT Pro	TTT Phe 150	GCC Ala	TGT Cys	GAC Asp	ATT Ile	TGT Cys 155	GGG Gly	AGG Arg	AAG Lys	TTT Phe	GCC Ala 160	480
AGG Arg	AGT Ser	GAT Asp	GAA Glu	CGC Arg 165	AAG Lys	AGG Arg	CAT His	ACC Thr	AAA Lys 170	ATC Ile	CAT	TTA Leu	AGA Arg	CAG Gln 175	AAG Lys	528
				AGT Ser												543

# (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 181 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg 10 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly 25 20 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe 60 55 Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys 70 Arg His Thr Lys Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Pro Val 95 90 Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His 110 105 100 Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Ser Met 125 120 115 Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His 140 130 135 Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala 155 150 Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys 175 170 165

# Asp Ser Arg Thr Ser 180 (2). INFORMATION FOR SEQ ID NO:45: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45: GAGGAGGAGG AGGGATCCAT GCTCGAGCTC CCCTATGCTT GCCCTG 46 (2) INFORMATION FOR SEQ ID NO:46: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46: 39: GAGGAGGAGA CCGGTATGGA TTTTGGTATG CCTCTTGCG (2) INFORMATION FOR SEQ ID NO:47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47: GAGGAGGAGA CCGGTGAGAA GCCCTATGCT TGCCCTGTCG AGTCCTGCGA TCGCCGC 57 (2) INFORMATION FOR SEQ ID NO:48: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

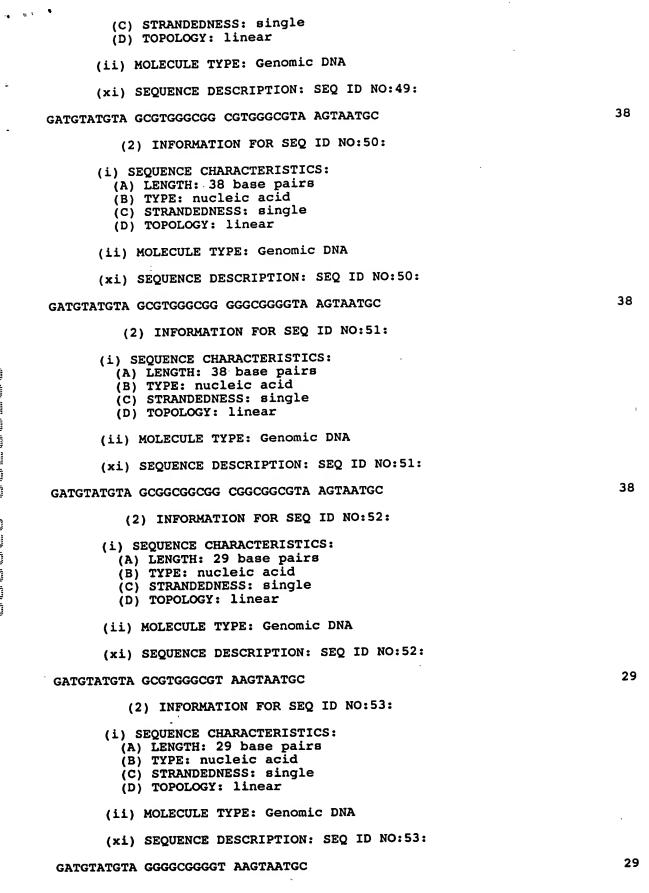
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

32

### GAGGAGGAGA CTAGTTCTAG AGTCCTTCTG TC

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid



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,	(2) INFORMATION FOR SEQ ID NO:54:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 29 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	·	
	(ii) MOLECULE TYPE: Genomic DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
	GATGTATGTA GCGTGGGCGT AAGTAATGC	29
	(2) INFORMATION FOR SEQ ID NO:55:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 41 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: Genomic DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
	GAGGAGGAGG AATTCCGACA TTTATAATGA ACGTGAATTG C	41
	(2) INFORMATION FOR SEQ ID NO:56:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 45 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	· ·	
	(ii) MOLECULE TYPE: Genomic DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
	TGCGCCCACG CCGCCCACGC GATGATTGGG AGCTTTTTTT GCACG	45
	(2) INFORMATION FOR SEQ ID NO:57:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 51 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: Genomic DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	٠
	TCGCGTGGGC GGCGTGGGCG CAAAAATTA TTATCATGGA TTCTAAAACG G	51
	(2) INFORMATION FOR SEQ ID NO:58:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 42 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	

10 .		
	(ii) MOLECULE TYPE: Genomic DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
	GAGGAGGAGG CGGCCGCAGG TAGATGAGAT GTGACGAACG TG	42
	(2) INFORMATION FOR SEQ ID NO:59:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 45 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: Genomic DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
	TGCCCCGCCC CCGCCCACGC GATGATTGGG AGCTTTTTTT GCACG	45
	(2) INFORMATION FOR SEQ ID NO:60:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: Genomic DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
	TCGCGTGGGC GGGGCGGGG CAAAAAATTA TTATCATGGA TTCTAAAACG G	51
	(2) INFORMATION FOR SEQ ID NO:61:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 18 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: Genomic DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
	GCGTGGGCGG CGTGGGCG	18
	(2) INFORMATION FOR SEQ ID NO:62:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 18 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: Genomic DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
	GCGTGGGCGG GGGCGGGG	18
	•	